

# SEQUENCE LISTING

<110> Genentech, Inc.  
Gao, Wei-Qiang

<120> HAIR CELL DISORDERS

<130> GENENT.035VPC

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<170> FastSEQ for Windows Version 4.0

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<212> PRT

<213> Homo sapiens

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Gly	Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	Ala	Leu	Pro	65	70	75	80
Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	Ala	Ala	Gly	Ser	Lys	85	90	95	
Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	100	105	110	
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Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	145	150	155	160
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Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	245	250	255	
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<222> (2)...(2008)

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act ttt ccc aaa ccc gat ccg agc cct tgg acc aaa ctc gcc tgc gcc 97
Thr Phe Pro Lys Pro Asp Pro Ser Pro Trp Thr Lys Leu Ala Cys Ala
      20             25             30

gag agc cgt ccg cgt aga gcg ctc cgt ctc cgg cga gat gtc cga gcg 145
Glu Ser Arg Pro Arg Arg Ala Leu Arg Leu Arg Arg Asp Val Arg Ala
      35             40             45

caa aga agg cag agg caa agg gaa ggg caa gaa gaa gga gcg agg ctc 193
Gln Arg Arg Gln Arg Gln Arg Glu Gly Gln Glu Glu Gly Ala Arg Leu
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cgg caa gaa gcc gga gtc cgc ggc ggg cag cca gag ccc agc ctt gcc 241
Arg Gln Glu Ala Gly Val Arg Gly Gly Gln Pro Glu Pro Ser Leu Ala
      65             70             75             80

tcc ccg att gaa aga gat gaa aag cca gga atc ggc tgc agg ttc caa 289
Ser Pro Ile Glu Arg Asp Glu Lys Pro Gly Ile Gly Cys Arg Phe Gln
      85             90             95

act agt cct tcg gtg tga aac cag ttc tga ata ctc ctc tct cag att 337
Thr Ser Pro Ser Val * Asn Gln Phe * Ile Leu Leu Ser Gln Ile
      100             105             110

caa gtg gtt caa gaa tgg gaa tga att gaa tcg aaa aaa caa acc aca 385
Gln Val Val Gln Glu Trp Glu * Ile Glu Ser Lys Lys Gln Thr Thr
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Lys Tyr Gln Asp Thr Lys Lys Ala Arg Glu Val Arg Thr Ser His *
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caa agc atc act ggc tga ttc tgg aga gta tat gtg caa agt gat cag 481
Gln Ser Ile Thr Gly * Phe Trp Arg Val Tyr Val Gln Ser Asp Gln
      145             150             155

caa att agg aaa tga cag tgc ctc tgc caa tat cac cat cgt gga atc 529
Gln Ile Arg Lys * Gln Cys Leu Cys Gln Tyr His His Arg Gly Ile
      160             165             170

aaa cga gat cat cac tgg tat gcc agc ctc aac tga agg agc ata tgt 577
Lys Arg Asp His His Trp Tyr Ala Ser Leu Asn * Arg Ser Ile Cys
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190 195 200	
tac ttc ttc atc tac atc tac atc cac cac tgg gac aag cca tct tgt	673
Tyr Phe Phe Ile Tyr Ile Tyr Ile His His Trp Asp Lys Pro Ser Cys	
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aaa atg tgc gga gaa gga gaa aac ttt ctg tgt gaa tgg agg gga gtg	721
Lys Met Cys Gly Glu Gly Glu Asn Phe Leu Cys Glu Trp Arg Gly Val	
220 225 230	
ctt cat ggt gaa aga cct ttc aaa ccc ctc gag ata ctt gtg caa gtg	769
Leu His Gly Glu Arg Pro Phe Lys Pro Leu Glu Ile Leu Val Gln Val	
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cca acc tgg att cac tgg agc aag atg tac tga gaa tgt gcc cat gaa	817
Pro Thr Trp Ile His Trp Ser Lys Met Tyr * Glu Cys Ala His Glu	
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agt cca aaa cca aga aaa ggc gga gga gct gta cca gaa gag agt gct	865
Ser Pro Lys Pro Arg Lys Gly Gly Gly Ala Val Pro Glu Ser Ala	
265 270 275	
gac cat aac cgg cat ctg cat cgc cct cct tgt ggt cgg cat cat gtg	913
Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg His His Val	
280 285 290 295	
tgt ggt ggc cta ctg caa aac caa gaa aca gcg gaa aaa gct gca tga	961
Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys Ala Ala *	
300 305 310	
ccg tct tcg gca gag cct tcg gtc tga acg aaa caa tat gat gaa cat	1009
Pro Ser Ser Ala Glu Pro Ser Val * Thr Lys Gln Tyr Asp Glu His	
315 320 325	
tgc caa tgg gcc tca cca tcc taa ccc acc ccc cga gaa tgt cca gct	1057
Cys Gln Trp Ala Ser Pro Ser * Pro Thr Pro Arg Glu Cys Pro Ala	
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ggg gaa tca ata cgt atc taa aaa cgt cat ctc cag tga gca tat tgt	1105
Gly Glu Ser Ile Arg Ile * Lys Arg His Leu Gln * Ala Tyr Cys	
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tga gag aga agc aga gac atc ctt ttc cac cag tca cta tac ttc cac	1153
* Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu Tyr Phe His	
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Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser * Pro Gln Leu Glu	
370 375 380	
caa cgg aca cac tga aag cat cct ttc cga aag cca ctc tgt aat cgt	1249
Gln Arg Thr His * Lys His Pro Phe Arg Lys Pro Leu Cys Asn Arg	
385 390 395	

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Asp Val Ile Arg Arg Lys Gln * Ala Gln Gln Pro Asn Trp Gly Pro	
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aag agg acg tct taa tgg cac agg agg ccc tcg tga atg taa cag ctt	1345
Lys Arg Thr Ser * Trp His Arg Arg Pro Ser * Met * Gln Leu	
415 420 425	
cct cag gca tgc cag aga aac ccc tga ttc cta ccg aga ctc tcc tca	1393
Pro Gln Ala Cys Gln Arg Asn Pro * Phe Leu Pro Arg Leu Ser Ser	
430 435 440	
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* * Lys Val Cys Val Ser His Asp His Pro Gly Ser Tyr Val Thr	
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Cys Arg Phe Pro His Ala Lys Leu Pro Gln Ile Ala Pro Phe Gly Asn	
460 465 470	
gtc tcc acc cgt gtc cag cat gac ggt gtc cat gcc ttc cat ggc ggt	1537
Val Ser Thr Arg Val Gln His Asp Gly Val His Ala Phe His Gly Gly	
475 480 485	
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Gln Pro Leu His Gly Arg Arg Glu Thr Ser Thr Ser Arg Asp Thr Thr	
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Lys Ala Ala Gly Glu Val * Pro Ser Pro Ser Ala Val Gln Leu	
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Leu Pro Pro Gln Pro Arg Ala * Gln * Gln Pro Pro Cys * Pro	
520 525 530	
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Leu Glu Asp Ser Gly Gly * Gly Val * Asn Asp Pro Arg Val Arg	
535 540 545	
gcc agc cca aga gcc tgt taa gaa act cgc caa tag ccg gcg ggc caa	1777
Ala Ser Pro Arg Ala Cys * Glu Thr Arg Gln * Pro Ala Gly Gln	
550 555 560	
aag aac caa gcc caa tgg cca cat tgc taa cag att gga agt gga cag	1825
Lys Asn Gln Ala Gln Trp Pro His Cys * Gln Ile Gly Ser Gly Gln	
565 570 575	
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Gln His Lys Leu Pro Glu Gln * Leu Arg Glu * Asn Arg Arg *	
580 585	
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Glu	Arg	Lys	Glu	Gly	Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Glu	Arg
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Gly	Ser	Gly	Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	Ala
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Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	Leu
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Arg	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys
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Glu	Ser	Asn	Glu	Ile	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	Gly	Ala	
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Tyr	Val	Ser	Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly
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Ala	Asn	Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr	Ser	His
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Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met
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Leu	Tyr	Gln	Lys	Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	Cys	Ile	Ala	Leu
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Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	Thr	Ser	Phe	Ser
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<220>  
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 <222> (3)...(2027)

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cct gcg ccg aga gcc gtc cgc gta gag cgc tcc gtc tcc ggc gag atg      95
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            20             25             30

tcc gag cgc aaa gaa ggc aga ggc aaa ggg aag ggc aag aag aag gag      143
  Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu
            35             40             45

cga ggc tcc ggc aag aag ccg gag tcc gcg gcg ggc agc cag agc cca      191
  Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro
            50             55             60

gcc ttg cct ccc caa ttg aaa gag atg aaa agc cag gaa tcg gct gca      239
  Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala
            65             70             75

ggg tcc aaa cta gtc ctt cgg tgt gaa acc agt tct gaa tac tcc tct      287
  Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser
            80             85             90             95

ctc aga ttc aag tgg ttc aag aat ggg aat gaa ttg aat cga aaa aac      335
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            100            105            110

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  Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu
            115            120            125

cgc att aac aaa gca tca ctg gct gat tct gga gag tat atg tgc aaa      431
  Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys
            130            135            140

gtg atc agc aaa tta gga aat gac agt gcc tct gcc aat atc acc atc      479
  Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile
            145            150            155

gtg gaa tca aac gag atc atc act ggt atg cca gcc tca act gaa gga      527
  Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly
            160            165            170            175

gca tat gtg tct tca gag tct ccc att aga ata tca gta tcc aca gaa      575
  Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu

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180										185					190					
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Gly	Ala	Asn	Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr	Ser					
195					200					205										
cat	ctt	gta	aaa	tgt	gcg	gag	aag	gag	aaa	act	ttc	tgt	gtg	aat	gga	671				
His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly					
210					215					220										
ggg	gag	tgc	ttc	atg	gtg	aaa	gac	ctt	tca	aac	ccc	tcg	aga	tac	ttg	719				
Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu					
225					230					235										
tgc	aag	tgc	cca	aat	gag	ttt	act	ggg	gat	cg	tgc	caa	aac	tac	gta	767				
Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val					
240					245					250					255					
atg	gcc	agc	ttc	tac	aag	cat	ctt	ggg	att	gaa	ttt	atg	gag	gcg	gag	815				
Met	Ala	Ser	Phe	Tyr	Lys	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ala	Glu					
260					265					270										
gag	ctg	tac	cag	aag	aga	gtg	ctg	acc	ata	acc	ggc	atc	tgc	atc	gcc	863				
Glu	Leu	Tyr	Gln	Lys	Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	Cys	Ile	Ala					
275					280					285										
ctc	ctt	gtg	gtc	ggc	atc	atg	tgt	gtg	gtg	gcc	tac	tgc	aaa	acc	aag	911				
Leu	Leu	Val	Val	Gly	Ile	Met	Cys	Val	Val	Ala	Tyr	Cys	Lys	Thr	Lys					
290					295					300										
aaa	cag	cgg	aaa	aag	ctg	cat	gac	cgt	ctt	cgg	cag	agc	ctt	cgg	tct	959				
Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	Arg	Leu	Arg	Gln	Ser	Leu	Arg	Ser					
305					310					315										
gaa	cga	aac	aat	atg	atg	aac	att	gcc	aat	ggg	cct	cac	cat	cct	aac	1007				
Glu	Arg	Asn	Asn	Met	Met	Asn	Ile	Ala	Asn	Gly	Pro	His	His	Pro	Asn					
320					325					330					335					
cca	ccc	ccc	gag	aat	gtc	cag	ctg	gtg	aat	caa	tac	gta	tct	aaa	aac	1055				
Pro	Pro	Pro	Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn					
340					345					350										
gtc	atc	tcc	agt	gag	cat	att	gtt	gag	aga	gaa	gca	gag	aca	tcc	ttt	1103				
Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	Thr	Ser	Phe					
355					360					365										
tcc	acc	agt	cac	tat	act	tcc	aca	gcc	cat	cac	tcc	act	act	gtc	acc	1151				
Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr	Thr	Val	Thr					
370					375					380										
cag	act	cct	agc	cac	agc	tgg	agc	aac	gga	cac	act	gaa	agc	atc	ctt	1199				
Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Leu					
385					390					395										
tcc	gaa	agc	cac	tct	gta	atc	gtg	atg	tca	tcc	gta	gaa	aac	agt	agg	1247				

Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg		
400					405					410					415		
cac	agc	agc	cca	act	ggg	ggc	cca	aga	gga	cgt	ctt	aat	ggc	aca	gga	1295	
His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	Thr	Gly		
				420					425					430			
ggc	cct	cgt	gaa	tgt	aac	agc	ttc	ctc	agg	cat	gcc	aga	gaa	acc	cct	1343	
Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	Glu	Thr	Pro		
			435					440					445				
gat	tcc	tac	cga	gac	tct	cct	cat	agt	gaa	agg	tat	gtg	tca	gcc	atg	1391	
Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser	Glu	Arg	Tyr	Val	Ser	Ala	Met		
		450					455					460					
acc	acc	ccg	gct	cgt	atg	tca	cct	gta	gat	ttc	cac	acg	cca	agc	tcc	1439	
Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp	Phe	His	Thr	Pro	Ser	Ser		
		465				470					475						
ccc	aaa	tcg	ccc	cct	tcg	gaa	atg	tct	cca	ccc	gtg	tcc	agc	atg	acg	1487	
Pro	Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	Met	Thr		
480				485					490					495			
gtg	tcc	atg	cct	tcc	atg	gcg	gtc	agc	ccc	ttc	atg	gaa	gaa	gag	aga	1535	
Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro	Phe	Met	Glu	Glu	Glu	Arg		
			500					505					510				
cct	cta	ctt	ctc	gtg	aca	cca	cca	agg	ctg	cgg	gag	aag	aag	ttt	gac	1583	
Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	Arg	Leu	Arg	Glu	Lys	Lys	Phe	Asp		
			515					520					525				
cat	cac	cct	cag	cag	ttc	agc	tcc	ttc	cac	cac	aac	ccc	gcg	cat	gac	1631	
His	His	Pro	Gln	Gln	Phe	Ser	Ser	Phe	His	His	Asn	Pro	Ala	His	Asp		
		530					535					540					
agt	aac	agc	ctc	cct	gct	agc	ccc	ttg	agg	ata	gtg	gag	gat	gag	gag	1679	
Ser	Asn	Ser	Leu	Pro	Ala	Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	Glu		
	545					550					555						
tat	gaa	acg	acc	caa	gag	tac	gag	cca	gcc	caa	gag	cct	gtt	aag	aaa	1727	
Tyr	Glu	Thr	Thr	Gln	Glu	Tyr	Glu	Pro	Ala	Gln	Glu	Pro	Val	Lys	Lys		
560				565					570					575			
ctc	gcc	aat	agc	cgg	cgg	gcc	aaa	aga	acc	aag	ccc	aat	ggc	cac	att	1775	
Leu	Ala	Asn	Ser	Arg	Arg	Ala	Lys	Arg	Thr	Lys	Pro	Asn	Gly	His	Ile		
			580					585					590				
gct	aac	aga	ttg	gaa	gtg	gac	agc	aac	aca	agc	tcc	cag	agc	agt	aac	1823	
Ala	Asn	Arg	Leu	Glu	Val	Asp	Ser	Asn	Thr	Ser	Ser	Gln	Ser	Ser	Asn		
			595					600					605				
tca	gag	agt	gaa	aca	gaa	gat	gaa	aga	gta	ggg	gaa	gat	acg	cct	ttc	1871	
Ser	Glu	Ser	Glu	Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	Thr	Pro	Phe		
		610					615					620					

ctg ggc ata cag aac ccc	ctg gca gcc agt ctt	gag gca aca cct gcc	1919
Leu Gly Ile Gln Asn Pro	Leu Ala Ala Ser Leu	Glu Ala Thr Pro Ala	
625	630	635	

ttc cgc ctg gct gac agc agg act aac cca	gca ggc cgc ttc tcg aca	1967
Phe Arg Leu Ala Asp Ser Arg Thr Asn Pro	Ala Gly Arg Phe Ser Thr	
640	650	655

cag gaa gaa atc cag gcc agg ctg tct agt gta att gct aac caa gac	2015
Gln Glu Glu Ile Gln Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp	
660	670

cct att gct gta taaaacctaa ataaacacat agattcacct gtaaaacttt	2067
Pro Ile Ala Val	
675	

atattatata ataaagtatt ccaccttaaa ttaaacaatt tattttatatt tagcagttct	2127
gcaaatagaa aacaggaaaa aaacttttat aaattaaata tatgtatgta aaaatgaaaa	2187
aaaaaaaaaa aa	2199

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 <212> PRT  
 <213> Homo sapiens

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Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala	
35	45
Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser	
50	60
Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys	
65	80
Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu	
85	95
Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys	
100	110
Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr	
115	125
Ile Val Glu Ser Asn Glu Ile Thr Gly Met Pro Ala Ser Thr Glu	
130	140
Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr	
145	160
Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Thr Thr Gly Thr	
165	175
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
180	190
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
195	205
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
210	220
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val	

225		230		235		240
Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met						
	245		250		255	
Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His						
	260		265		270	
Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn						
	275		280		285	
Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln						
	290		295		300	
Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile						
305		310		315		320
Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser						
	325		330		335	
Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp						
	340		345		350	
Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile						
	355		360		365	
Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly						
	370		375		380	
Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser						
385		390		395		400
Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro						
	405		410		415	
His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser						
	420		425		430	
Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu						
	435		440		445	
Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Lys Pro Ser Met Ala						
	450		455		460	
Val Ser Pro Phe Met Glu Glu Arg Pro Leu Leu Leu Val Thr Pro						
465		470		475		480
Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser						
	485		490		495	
Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser						
	500		505		510	
Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr						
	515		520		525	
Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala						
	530		535		540	
Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp						
545		550		555		560
Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp						
	565		570		575	
Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu						
	580		585		590	
Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg						
	595		600		605	
Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala Arg						
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Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val						
625		630		635		

<210> 6

<211> 2460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (461)...(2371)

<400> 6

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cgggctcgcg cggaggccag gagctgagcg gcggcggtcg ccgacgatg ggagcgtgag 120
caggacggtg ataacctctc cccgatcggg ttgcgagggc gccgggcaga ggccaggacg 180
cgagccgcca gcggcgggac ccatcgacga cttcccgggg cgacaggagc agccccgaga 240
gccagggcga gcgcccgttc caggtggccg gaccgcccgc cgcgtccgcg ccgcgctccc 300
tgcaggcaac gggagacgcc cccgcgcagc gcgagcgcct cagcgcggcc gctcgtcttc 360
cccacgaggg gacaaacttt tcccaaacc gatccgagcc cttggaccaa actcgcctgc 420
cccagagacc gtccgcgtag agcgtctcgt ctccggcgag atg tcc gag cgc aaa 475
                               Met Ser Glu Arg Lys
                               1       5
```

```
gaa ggc aga ggc aaa ggg aag ggc aag aag aag gag cga ggc tcc ggc 523
Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu Arg Gly Ser Gly
                10                15                20
```

```
aag aag ccg gag tcc gcg gcg ggc agc cag agc cca gcc ttg cct ccc 571
Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro
                25                30                35
```

```
caa ttg aaa gag atg aaa agc cag gaa tcg gct gca ggt tcc aaa cta 619
Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
                40                45                50
```

```
gtc ctt cgg tgt gaa acc agt tct gaa tac tcc tct ctc aga ttc aag 667
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys
                55                60                65
```

```
tgg ttc aag aat ggg aat gaa ttg aat cga aaa aac aaa cca caa aat 715
Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn
                70                75                80                85
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atc aag ata caa aaa aag cca ggg aag tca gaa ctt cgc att aac aaa 763
Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys
                90                95                100
```

```
gca tca ctg gct gat tct gga gag tat atg tgc aaa gtg atc agc aaa 811
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys
                105                110                115
```

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tta gga aat gac agt gcc tct gcc aat atc acc atc gtg gaa tca aac 859
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn
                120                125                130
```

```
gag atc atc act ggt atg cca gcc tca act gaa gga gca tat gtg tct 907
Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser
                135                140                145
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tca gag tct ccc att aga ata tca gta tcc aca gaa gga gca aat act	955
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn Thr	
150 155 160 165	
tct tca tct aca tct aca tcc acc act ggg aca agc cat ctt gta aaa	1003
Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys	
170 175 180	
tgt gcg gag aag gag aaa act ttc tgt gtg aat gga ggg gag tgc ttc	1051
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe	
185 190 195	
atg gtg aaa gac ctt tca aac ccc tcg aga tac ttg tgc aag tgc cca	1099
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro	
200 205 210	
aat gag ttt act ggt gat cgc tgc caa aac tac gta atg gcc agc ttc	1147
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe	
215 220 225	
tac aag gcg gag gag ctg tac cag aag aga gtg ctg acc ata acc ggc	1195
Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly	
230 235 240 245	
atc tgc atc gcc ctc ctt gtg gtc ggc atc atg tgt gtg gtg gcc tac	1243
Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr	
250 255 260	
tgc aaa acc aag aaa cag cgg aaa aag ctg cat gac cgt ctt cgg cag	1291
Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln	
265 270 275	
agc ctt cgg tct gaa cga aac aat atg atg aac att gcc aat ggg cct	1339
Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile Ala Asn Gly Pro	
280 285 290	
cac cat cct aac cca ccc ccc gag aat gtc cag ctg gtg aat caa tac	1387
His His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr	
295 300 305	
gta tct aaa aac gtc atc tcc agt gag cat att gtt gag aga gaa gca	1435
Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala	
310 315 320 325	
gag aca tcc ttt tcc acc agt cac tat act tcc aca gcc cat cac tcc	1483
Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser	
330 335 340	
act act gtc acc cag act cct agc cac agc tgg agc aac gga cac act	1531
Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr	
345 350 355	
gaa agc atc ctt tcc gaa agc cac tct gta atc gtg atg tca tcc gta	1579
Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val	
360 365 370	

gaa aac agt agg cac agc agc cca act ggg ggc cca aga gga cgt ctt	1627
Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu	
375 380 385	
aat ggc aca gga ggc cct cgt gaa tgt aac agc ttc ctc agg cat gcc	1675
Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala	
390 395 400 405	
aga gaa acc cct gat tcc tac cga gac tct cct cat agt gaa agg tat	1723
Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg Tyr	
410 415 420	
gtg tca gcc atg acc acc ccg gct cgt atg tca cct gta gat ttc cac	1771
Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe His	
425 430 435	
acg cca agc tcc ccc aaa tcg ccc cct tcg gaa atg tct cca ccc gtg	1819
Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val	
440 445 450	
tcc agc atg acg gtg tcc aag cct tcc atg gcg gtc agc ccc ttc atg	1867
Ser Ser Met Thr Val Ser Lys Pro Ser Met Ala Val Ser Pro Phe Met	
455 460 465	
gaa gaa gag aga cct cta ctt ctc gtg aca cca cca agg ctg cgg gag	1915
Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu	
470 475 480 485	
aag aag ttt gac cat cac cct cag cag ttc agc tcc ttc cac cac aac	1963
Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe His His Asn	
490 495 500	
ccc gcg cat gac agt aac agc ctc cct gct agc ccc ttg agg ata gtg	2011
Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser Pro Leu Arg Ile Val	
505 510 515	
gag gat gag gag tat gaa acg acc caa gag tac gag cca gcc caa gag	2059
Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu	
520 525 530	
cct gtt aag aaa ctc gcc aat agc cgg cgg gcc aaa aga acc aag ccc	2107
Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro	
535 540 545	
aat ggc cac att gct aac aga ttg gaa gtg gac agc aac aca agc tcc	2155
Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser Asn Thr Ser Ser	
550 555 560 565	
cag agc agt aac tca gag agt gaa aca gaa gat gaa aga gta ggt gaa	2203
Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val Gly Glu	
570 575 580	
gat acg cct ttc ctg ggc ata cag aac ccc ctg gca gcc agt ctt gag	2251
Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser Leu Glu	

585										590										595										
gca	aca	cct	gcc	ttc	cgc	ctg	gct	gac	agc	agg	act	aac	cca	gca	ggc	2299														
Ala	Thr	Pro	Ala	Phe	Arg	Leu	Ala	Asp	Ser	Arg	Thr	Asn	Pro	Ala	Gly															
600					605					610																				
cgc	ttc	tcg	aca	cag	gaa	gaa	atc	cag	gcc	agg	ctg	tct	agt	gta	att	2347														
Arg	Phe	Ser	Thr	Gln	Glu	Glu	Ile	Gln	Ala	Arg	Leu	Ser	Ser	Val	Ile															
615					620					625																				
gct	aac	caa	gac	cct	att	gct	gta	taaaacctaa	ataaacacat	agattcacct	2401																			
Ala	Asn	Gln	Asp	Pro	Ile	Ala	Val																							
630					635																									
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<211> 241

<212> PRT

<213> Homo sapiens

<400> 7

Met	Ser	Glu	Arg	Lys	Glu	Gly	Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys
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Glu	Arg	Gly	Ser	Gly	Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser
			20					25					30		
Pro	Ala	Leu	Pro	Pro	Gln	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	Ala
		35					40					45			
Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser
	50					55					60				
Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys
65					70					75					80
Asn	Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu
				85					90					95	
Leu	Arg	Ile	Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys
			100					105					110		
Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Thr
		115					120					125			
Ile	Val	Glu	Ser	Asn	Glu	Ile	Ile	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu
	130					135					140				
Gly	Ala	Tyr	Val	Ser	Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr
145					150					155					160
Glu	Gly	Ala	Asn	Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr
				165					170					175	
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn
			180					185					190		
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr
		195					200					205			
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr
	210					215					220				
Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro
225					230					235					240
Glu															



<210> 8  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (493)...(1215)

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 ggcgaggagt tccccgaaac ttgttggaac tccgggctcg cgcggaggcc aggagctgag 120  
 cggcggcggc tgccggacga tgggagcgtg agcaggacgg tgataacctc tccccgatcg 180  
 ggttgcgagg gcgcggggca gaggccagga cgcgagccgc cagcggcggg acccatcgac 240  
 gacttcccgg ggcgacagga gcagccccga gagccagggc gagcggccgt tccaggtggc 300  
 cggaccgccc gccgcgtccg cgccgcgctc cctgcaggca acgggagacg cccccgcgca 360  
 gcgcgagcgc ctacgcggc cgctcgcctc tccccatcga gggacaaaact tttcccaaac 420  
 ccgatccgag cccttgagcc aaactcgcct gcgccgagag ccgtccgcgt agagcgtccc 480  
 gtctccggcg ag atg tcc gag cgc aaa gaa ggc aga ggc aaa ggg aag ggc 531  
                   Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly  
                   1                  5                  10  
 aag aag aag gag cga ggc tcc ggc aag aag ccg gag tcc gcg gcg ggc 579  
 Lys Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly  
                   15                  20                  25  
 agc cag agc cca gcc ttg cct ccc caa ttg aaa gag atg aaa agc cag 627  
 Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln  
                   30                  35                  40                  45  
 gaa tcg gct gca ggt tcc aaa cta gtc ctt cgg tgt gaa acc agt tct 675  
 Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser  
                   50                  55                  60  
 gaa tac tcc tct ctc aga ttc aag tgg ttc aag aat ggg aat gaa ttg 723  
 Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu  
                   65                  70                  75  
 aat cga aaa aac aaa cca caa aat atc aag ata caa aaa aag cca ggg 771  
 Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly  
                   80                  85                  90  
 aag tca gaa ctt cgc att aac aaa gca tca ctg gct gat tct gga gag 819  
 Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu  
                   95                  100                  105  
 tat atg tgc aaa gtg atc agc aaa tta gga aat gac agt gcc tct gcc 867  
 Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala  
                   110                  115                  120                  125  
 aat atc acc atc gtg gaa tca aac gag atc atc act ggt atg cca gcc 915  
 Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala  
                   130                  135                  140

tca act gaa gga gca tat gtg tct tca gag tct ccc att aga ata tca	963
Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser	
145 150 155	
gta tcc aca gaa gga gca aat act tct tca tct aca tct aca tcc acc	1011
Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr	
160 165 170	
act ggg aca agc cat ctt gta aaa tgt gcg gag aag gag aaa act ttc	1059
Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe	
175 180 185	
tgt gtg aat gga ggg gag tgc ttc atg gtg aaa gac ctt tca aac ccc	1107
Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro	
190 195 200 205	
tcg aga tac ttg tgc aag tgc cca aat gag ttt act ggt gat cgc tgc	1155
Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys	
210 215 220	
caa aac tac gta atg gcc agc ttc tac agt acg tcc act ccc ttt ctg	1203
Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu	
225 230 235	
tct ctg cct gaa taggagcatg ctcagttggt gctgctttct tgttgctgca	1255
Ser Leu Pro Glu	
240	
tctcccctca gattccacct agagctagat gtgtcttacc agatctaata ttgactgcct	1315
ctgcctgtcg catgagaaca ttaacaaaag caattgtatt acttcctctg ttcgcgacta	1375
gttggctctg agatactaata aggtgtgtga ggctccggat gtttctggaa ttgatattga	1435
atgatgtgat acaaattgat agtcaatatc aagcagtga atatgataat aaaggcattt	1495
caaagtctca cttttattga taaaataaaa atcattctac tgaacagtcc atcttcttta	1555
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<211> 420

<212> PRT

<213> Homo sapiens

<400> 9

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Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala	
35 40 45	
Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser	
50 55 60	
Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys	
65 70 75 80	
Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu	
85 90 95	

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys  
 100 105 110  
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr  
 115 120 125  
 Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu  
 130 135 140  
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr  
 145 150 155 160  
 Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr  
 165 170 175  
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 180 185 190  
 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 195 200 205  
 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
 210 215 220  
 Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val  
 225 230 235 240  
 Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met  
 245 250 255  
 Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His  
 260 265 270  
 Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn  
 275 280 285  
 Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln  
 290 295 300  
 Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile  
 305 310 315 320  
 Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser  
 325 330 335  
 Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp  
 340 345 350  
 Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile  
 355 360 365  
 Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly  
 370 375 380  
 Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser  
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 405 410 415  
 His Ser Glu Arg  
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<212> DNA

<213> Homo sapiens

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gagcggcggc ggctgccgga cgatgggagc gtgagcagga cggtgataac ctctccccga 180  
tcgggttgcg agggcgcccg gcagaggcca ggacgcgagc cgccagcggc gggacccatc 240  
gacgacttcc cggggcgaca ggagcagccc cgagagccag ggcgagcgcc cgttccaggt 300  
ggccggaccg cccgcccgtt ccgcgcgcgc ctccctgcag gcaacgggag acgccccgcg 360  
gcagcgcgag cgcctcagcg cggccgctcg ctctcccat cgagggacaa acttttccca 420  
aaccgatcc gagcccttgg accaaactcg cctgcgccga gagccgtccg cgtagagcgc 480  
tccgtctccg gcgag atg tcc gag cgc aaa gaa ggc aga ggc aaa ggg aag 531

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys  
1 5 10

ggc aag aag aag gag cga ggc tcc ggc aag aag ccg gag tcc gcg gcg 579  
Gly Lys Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala  
15 20 25

ggc agc cag agc cca gcc ttg cct ccc caa ttg aaa gag atg aaa agc 627  
Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser  
30 35 40

cag gaa tcg gct gca ggt tcc aaa cta gtc ctt cgg tgt gaa acc agt 675  
Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser  
45 50 55 60

tct gaa tac tcc tct ctc aga ttc aag tgg ttc aag aat ggg aat gaa 723  
Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu  
65 70 75

ttg aat cga aaa aac aaa cca caa aat atc aag ata caa aaa aag cca 771  
Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro  
80 85 90

ggg aag tca gaa ctt cgc att aac aaa gca tca ctg gct gat tct gga 819  
Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly  
95 100 105

gag tat atg tgc aaa gtg atc agc aaa tta gga aat gac agt gcc tct 867  
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser  
110 115 120

gcc aat atc acc atc gtg gaa tca aac gag atc atc act ggt atg cca 915  
Ala Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro  
125 130 135 140

gcc tca act gaa gga gca tat gtg tct tca gag tct ccc att aga ata 963  
Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile  
145 150 155

tca gta tcc aca gaa gga gca aat act tct tca tct aca tct aca tcc 1011  
Ser Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser  
160 165 170

acc act ggg aca agc cat ctt gta aaa tgt gcg gag aag gag aaa act 1059  
Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr  
175 180 185

ttc tgt gtg aat gga ggg gag tgc ttc atg gtg aaa gac ctt tca aac	1107
Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn	
190 195 200	
ccc tcg aga tac ttg tgc aag tgt cca aat gag ttt act ggt gat cgc	1155
Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg	
205 210 215 220	
tgc caa aac tac gta atg gcc agc ttc tac aag gcg gag gag ctg tac	1203
Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr	
225 230 235	
cag aag aga gtg ctg acc ata acc ggc atc tgc atc gcc ctc ctt gtg	1251
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	
240 245 250	
gtc ggc atc atg tgt gtg gtg gcc tac tgc aaa acc aag aaa cag cgg	1299
Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg	
255 260 265	
aaa aag ctg cat gac cgt ctt cgg cag agc ctt cgg tct gaa cga aac	1347
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn	
270 275 280	
aat atg atg aac att gcc aat ggg cct cac cat cct aac cca ccc ccc	1395
Asn Met Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro	
285 290 295 300	
gag aat gtc cag ctg gtg aat caa tac gta tct aaa aac gtc atc tcc	1443
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser	
305 310 315	
agt gag cat att gtt gag aga gaa gca gag aca tcc ttt tcc acc agt	1491
Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser	
320 325 330	
cac tat act tcc aca gcc cat cac tcc act act gtc acc cag act cct	1539
His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro	
335 340 345	
agc cac agc tgg agc aac gga cac act gaa agc atc ctt tcc gaa agc	1587
Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser	
350 355 360	
cac tct gta atc gtg atg tca tcc gta gaa aac agt agg cac agc agc	1635
His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser	
365 370 375 380	
cca act ggg ggc cca aga gga cgt ctt aat ggc aca gga ggc cct cgt	1683
Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg	
385 390 395	
gaa tgt aac agc ttc ctc agg cat gcc aga gaa acc cct gat tcc tac	1731
Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr	
400 405 410	

cga gac tct cct cat agt gaa agg taaaaccgaa ggcaaagcta ctgcagagga 1785  
 Arg Asp Ser Pro His Ser Glu Arg  
 415 420

gaaactcagt cagagaatcc ctgtgagcac ctgcggtctc acctcaggaa atctactcta 1845  
 atcagaataa ggggcggcag ttacctgttc taggagtgtc cctagttgat gaagtcactc 1905  
 ctttgtttga cggaacttat ttcttctgag cttctctcgt cgtcccagtg actgacaggc 1965  
 aacagactct taaagagctg ggatgctttg atgcggaagg tgcagcacat ggagtttcca 2025  
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 <213> Homo sapiens

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 Lys Ala Pro Gln Lys Ser Tyr Ser Ser Glu Thr Leu Lys Ala Tyr  
 35 40 45  
 Asp Gln Asp Ala Arg Leu Ala Tyr Gly Ser Arg Val Lys Asp Ile Val  
 50 55 60  
 Pro Gln Glu Ala Glu Glu Phe Cys Arg Thr Gly Ala Asn Phe Thr Leu  
 65 70 75 80  
 Arg Glu Leu Gly Leu Glu Glu Val Thr Pro Pro His Gly Thr Leu Tyr  
 85 90 95  
 Arg Thr Asp Ile Gly Leu Pro His Cys Gly Tyr Ser Met Gly Ala Gly  
 100 105 110  
 Ser Asp Ala Asp Met Glu Ala Asp Thr Val Leu Ser Pro Glu His Pro  
 115 120 125  
 Val Arg Leu Trp Gly Arg Ser Thr Arg Ser Gly Arg Ser Ser Cys Leu  
 130 135 140  
 Ser Ser Arg Ala Asn Ser Asn Leu Thr Leu Thr Asp Thr Glu His Glu  
 145 150 155 160  
 Asn Thr Glu Thr Asp His Pro Gly Gly Leu Gln Asn His Ala Arg Leu  
 165 170 175  
 Arg Thr Pro Pro Pro Leu Ser His Ala His Thr Pro Asn Gln His  
 180 185 190  
 His Ala Ala Ser Ile Asn Ser Leu Asn Arg Gly Asn Phe Thr Pro Arg  
 195 200 205  
 Ser Asn Pro Ser Pro Ala Pro Thr Asp His Ser Leu Ser Gly Glu Pro  
 210 215 220  
 Pro Ala Gly Gly Ala Gln Glu Pro Ala His Ala Gln Glu Asn Trp Leu  
 225 230 235 240  
 Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg Asn Leu Gly Lys Gln Pro  
 245 250 255

Phe	Leu	Gly	Thr	Leu	Gln	Asp	Asn	Leu	Ile	Glu	Met	Asp	Ile	Leu	Gly	260	265	270
Ala	Ser	Arg	His	Asp	Gly	Ala	Tyr	Ser	Asp	Gly	His	Phe	Leu	Phe	Lys	275	280	285
Pro	Gly	Gly	Thr	Ser	Pro	Leu	Phe	Cys	Thr	Thr	Ser	Pro	Gly	Tyr	Pro	290	295	300
Leu	Thr	Ser	Ser	Thr	Val	Tyr	Ser	Pro	Pro	Pro	Arg	Pro	Leu	Pro	Arg	305	310	315
Ser	Thr	Phe	Ala	Arg	Pro	Ala	Phe	Asn	Leu	Lys	Lys	Pro	Ser	Lys	Tyr	320	325	330
Cys	Asn	Trp	Lys	Cys	Ala	Ala	Leu	Ser	Ala	Ile	Val	Ile	Ser	Ala	Thr	335	340	345
Leu	Val	Ile	Leu	Leu	Ala	Tyr	Phe	Val	Ala	Met	His	Leu	Phe	Gly	Leu	350	355	360
Asn	Trp	His	Leu	Gln	Pro	Met	Glu	Gly	Gln	Met	Tyr	Glu	Ile	Thr	Glu	365	370	375
Asp	Thr	Ala	Ser	Ser	Trp	Pro	Val	Pro	Thr	Asp	Val	Ser	Leu	Tyr	Pro	380	385	390
Ser	Gly	Gly	Thr	Gly	Leu	Glu	Thr	Pro	Asp	Arg	Lys	Gly	Lys	Gly	Thr	395	400	405
Thr	Glu	Gly	Lys	Pro	Ser	Ser	Phe	Phe	Pro	Glu	Asp	Ser	Phe	Ile	Asp	410	415	420
Ser	Gly	Glu	Ile	Asp	Val	Gly	Arg	Arg	Ala	Ser	Gln	Lys	Ile	Pro	Pro	425	430	435
Gly	Thr	Phe	Trp	Arg	Ser	Gln	Val	Phe	Ile	Asp	His	Pro	Val	His	Leu	440	445	450
Lys	Phe	Asn	Val	Ser	Leu	Gly	Lys	Ala	Ala	Leu	Val	Gly	Ile	Tyr	Gly	455	460	465
Arg	Lys	Gly	Leu	Pro	Ser	His	Thr	Gln	Phe	Asp	Phe	Val	Glu	Leu		470	475	480
Leu	Asp	Gly	Arg	Leu	Leu	Thr	Gln	Glu	Ala	Arg	Ser	Leu	Glu	Gly		485	490	495
Thr	Pro	Arg	Gln	Ser	Arg	Gly	Thr	Val	Pro	Pro	Ser	Ser	His	Glu	Thr	500	505	510
Gly	Phe	Ile	Gln	Tyr	Leu	Asp	Ser	Gly	Ile	Trp	His	Leu	Ala	Phe	Tyr	515	520	525
Asn	Asp	Gly	Lys	Glu	Ser	Glu	Val	Val	Ser	Phe	Leu	Thr	Thr	Ala	Ile	530	535	540
Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	Ala	Ala	545	550	555
Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	560	565	570
Leu	Arg	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	575	580	585
Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	590	595	600
Arg	Ile	Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	605	610	615
Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Thr	Ile	620	625	630
Val	Glu	Ser	Asn	Glu	Ile	Ile	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	Gly	635	640	645
Ala	Tyr	Val	Ser	Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	650	655	660
Gly	Ala	Asn	Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr	Ser	665	670	675

690		695		700
His Leu Val Lys Cys	Ala Glu Lys Glu Lys Thr	Phe Cys Val Asn Gly		
705	710	715		720
Gly Glu Cys Phe Met	Val Lys Asp Leu Ser Asn Pro	Ser Arg Tyr Leu		
	725	730		735
Cys Lys Cys Pro Asn	Glu Phe Thr Gly Asp Arg Cys	Gln Asn Tyr Val		
	740	745		750
Met Ala Ser Phe Tyr	Ser Thr Ser Thr Pro Phe Leu	Ser Leu Pro Glu		
	755	760		765

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 <212> DNA  
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<400> 12

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cagggccac ggacattgct gactcttcag aacgtgctga catggagcca ggtagactga	180
aattatcatg tgtccaaatt aaaattgcat acttcaagga ttatttgaag gactattctt	240
agaccctttt aagaagattt aaagaaaaac cactcggccc tgagtgcggc gaggaccctg	300
tttgtggatg tggaggagcg cgggcccggag gcc atg gac gtg aag gag agg aag	354
	Met Asp Val Lys Glu Arg Lys
	1 5
cct tac cgc tcg ctg acc cgg cgc cgc gac gcc gag cgc cgc tac acc	402
Pro Tyr Arg Ser Leu Thr Arg Arg Arg Asp Ala Glu Arg Arg Tyr Thr	
	10 15 20
agc tcg tcc gcg gac agc gag gag ggc aaa gcc ccg cag aaa tcg tac	450
Ser Ser Ser Ala Asp Ser Glu Glu Gly Lys Ala Pro Gln Lys Ser Tyr	
	25 30 35
agc tcc agc gag acc ctg aag gcc tac gac cag gac gcc cgc cta gcc	498
Ser Ser Ser Glu Thr Leu Lys Ala Tyr Asp Gln Asp Ala Arg Leu Ala	
	40 45 50 55
tat ggc agc cgc gtc aag gac att gtg ccg cag gag gcc gag gaa ttc	546
Tyr Gly Ser Arg Val Lys Asp Ile Val Pro Gln Glu Ala Glu Glu Phe	
	60 65 70
tgc cgc aca ggt gcc aac ttc acc ctg cgg gag ctg ggg ctg gaa gaa	594
Cys Arg Thr Gly Ala Asn Phe Thr Leu Arg Glu Leu Gly Leu Glu Glu	
	75 80 85
gta acg ccc cct cac ggg acc ctg tac cgg aca gac att ggc ctc ccc	642
Val Thr Pro Pro His Gly Thr Leu Tyr Arg Thr Asp Ile Gly Leu Pro	
	90 95 100
cac tgc ggc tac tcc atg ggg gct ggc tct gat gcc gac atg gag gct	690



His	Cys	Gly	Tyr	Ser	Met	Gly	Ala	Gly	Ser	Asp	Ala	Asp	Met	Glu	Ala		
105						110					115						
gac	acg	gtg	ctg	tcc	cct	gag	cac	ccc	gtg	cgt	ctg	tgg	ggc	cgg	agc	738	
Asp	Thr	Val	Leu	Ser	Pro	Glu	His	Pro	Val	Arg	Leu	Trp	Gly	Arg	Ser		
120					125					130					135		
aca	cgg	tca	ggg	cgc	agc	tcc	tgc	ctg	tcc	agc	cgg	gcc	aat	tcc	aat	786	
Thr	Arg	Ser	Gly	Arg	Ser	Ser	Cys	Leu	Ser	Ser	Arg	Ala	Asn	Ser	Asn		
				140					145					150			
ctc	aca	ctc	acc	gac	acc	gag	cat	gaa	aac	act	gag	act	gat	cat	ccg	834	
Leu	Thr	Leu	Thr	Asp	Thr	Glu	His	Glu	Asn	Thr	Glu	Thr	Asp	His	Pro		
			155					160					165				
ggc	ggc	ctg	cag	aac	cac	gcg	cgg	ctc	cgg	acg	ccg	ccg	ccg	ccg	ctc	882	
Gly	Gly	Leu	Gln	Asn	His	Ala	Arg	Leu	Arg	Thr	Pro	Pro	Pro	Pro	Leu		
		170					175					180					
tcg	cac	gcc	cac	acc	ccc	aac	cag	cac	cac	gcg	gcc	tcc	att	aac	tcc	930	
Ser	His	Ala	His	Thr	Pro	Asn	Gln	His	His	Ala	Ala	Ser	Ile	Asn	Ser		
		185				190					195						
ctg	aac	cgg	ggc	aac	ttc	acg	ccg	agg	agc	aac	ccc	agc	ccg	gcc	ccc	978	
Leu	Asn	Arg	Gly	Asn	Phe	Thr	Pro	Arg	Ser	Asn	Pro	Ser	Pro	Ala	Pro		
200					205					210					215		
acg	gac	cac	tcg	ctc	tcc	gga	gag	ccc	cct	gcc	ggc	ggc	gcc	cag	gag	1026	
Thr	Asp	His	Ser	Leu	Ser	Gly	Glu	Pro	Pro	Ala	Gly	Gly	Ala	Gln	Glu		
				220					225					230			
cct	gcc	cac	gcc	cag	gag	aac	tgg	ctg	ctc	aac	agc	aac	atc	ccc	ctg	1074	
Pro	Ala	His	Ala	Gln	Glu	Asn	Trp	Leu	Leu	Asn	Ser	Asn	Ile	Pro	Leu		
			235				240						245				
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aac	ctc	att	gag	atg	gac	att	ctc	ggc	gcc	tcc	cgc	cat	gat	ggg	gct	1170	
Asn	Leu	Ile	Glu	Met	Asp	Ile	Leu	Gly	Ala	Ser	Arg	His	Asp	Gly	Ala		
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tac	agt	gac	ggg	cac	ttc	ctc	ttc	aag	cct	gga	ggc	acc	tcc	ccg	ctc	1218	
Tyr	Ser	Asp	Gly	His	Phe	Leu	Phe	Lys	Pro	Gly	Gly	Thr	Ser	Pro	Leu		
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ttc	tgc	acc	aca	tca	cca	ggg	tac	cca	ctg	acg	tcc	agc	aca	gtg	tac	1266	
Phe	Cys	Thr	Thr	Ser	Pro	Gly	Tyr	Pro	Leu	Thr	Ser	Ser	Thr	Val	Tyr		
				300					305					310			
tct	cct	ccg	ccc	cga	ccc	ctg	ccc	cgc	agc	acc	ttc	gcc	cgg	ccg	gcc	1314	
Ser	Pro	Pro	Pro	Arg	Pro	Leu	Pro	Arg	Ser	Thr	Phe	Ala	Arg	Pro	Ala		
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Phe Asn Leu Lys Lys Pro Ser Lys Tyr Cys Asn Trp Lys Cys Ala Ala	
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Leu Ser Ala Ile Val Ile Ser Ala Thr Leu Val Ile Leu Leu Ala Tyr	
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Phe Val Ala Met His Leu Phe Gly Leu Asn Trp His Leu Gln Pro Met	
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Glu Gly Gln Met Tyr Glu Ile Thr Glu Asp Thr Ala Ser Ser Trp Pro	
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Val Pro Thr Asp Val Ser Leu Tyr Pro Ser Gly Gly Thr Gly Leu Glu	
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Thr Pro Asp Arg Lys Gly Lys Gly Thr Thr Glu Gly Lys Pro Ser Ser	
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Phe Phe Pro Glu Asp Ser Phe Ile Asp Ser Gly Glu Ile Asp Val Gly	
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Val Phe Ile Asp His Pro Val His Leu Lys Phe Asn Val Ser Leu Gly	
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Lys Ala Ala Leu Val Gly Ile Tyr Gly Arg Lys Gly Leu Pro Pro Ser	
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His Thr Gln Phe Asp Phe Val Glu Leu Leu Asp Gly Arg Arg Leu Leu	
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Thr Gln Glu Ala Arg Ser Leu Glu Gly Thr Pro Arg Gln Ser Arg Gly	
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Ser Gly Ile Trp His Leu Ala Phe Tyr Asn Asp Gly Lys Glu Ser Glu	
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Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg	
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Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys	
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Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile	
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Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu	
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Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn	
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Ser Thr Pro Phe Leu Ser Leu Pro Glu	

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Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu								
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